

		TM1
hASIC1a	MELKAE <sup>A</sup> EEEEVGGVQPVSIQAFASSSTLHGLAHIFSYERLSLKRALWALCFLGSLAVLLCV	
mASIC1a	MELKTE <sup>T</sup> EEEEVGGVQPVSIQAFASSSTLHGLAHIFSYERLSLKRALWALCFLGSLAVLLCV	
	70	
hASIC1a	CTERVQYYF <sup>H</sup> YHHVTKLDEVAASQLTFPAVTLCNLNEFRFSQVSKNDLYHAGELLALLNN	
mASIC1a	CTERVQYYF <sup>C</sup> YHHVTKLDEVAASQLTFPAVTLCNLNEFRFSQVSKNDLYHAGELLALLNN	
hASIC1a	RYEIPDTQMADEKQLEILQDKANFRSFKPKPFNMREFYDRAGHDIRDMLLSCHFRGE <sup>V</sup> C	
mASIC1a	RYEIPDTQMADEKQLEILQDKANFRSFKPKPFNMREFYDRAGHDIRDMLLSCHFRGE <sup>A</sup> CS	
hASIC1a	AEDFKVVFTRYGKCYTFNSGR <sup>R</sup> DGRPRLKTMKGGTGNGLEIMLDIQQDEYLPVWGETDETS	
mASIC1a	AEDFKVVFTRYGKCYTFNSGR <sup>Q</sup> DGRPRLKTMKGGTGNGLEIMLDIQQDEYLPVWGETDETS	
		285
hASIC1a	FEAGIKVQIHSQDEPPFIDQLGFGVAPGFQTFV <sup>A</sup> CQEQRLIYLP <sup>P</sup> PWGTCKAVTMDSDLD	
mASIC1a	FEAGIKVQIHSQDEPPFIDQLGFGVAPGFQTFV <sup>S</sup> CQEQRLIYLP <sup>S</sup> PWGT <sup>C</sup> NAV <sup>T</sup> MDS--D	
hASIC1a	FFDSYSITACRIDCETRYLVENCNCRMVHMPGDAPYCTPEQYKECADPALDFLVEKDQEY	
mASIC1a	FFDSYSITACRIDCETRYLVENCNCRMVHMPGDAPYCTPEQYKECADPALDFLVEKDQEY	
hASIC1a	CVCEMPCNLTRYGKELSMVKIPSKASAKYLAKKFNKSEQYIGENILVLDIFFEVLNYETI	
mASIC1a	CVCEMPCNLTRYGKELSMVKIPSKASAKYLAKKFNKSEQYIGENILVLDIFFEVLNYETI	
		TM2
hASIC1a	EQKKAYEIA <sup>G</sup> LLGDIGGQMG <sup>L</sup> FIGASILT <sup>V</sup> LELFDYAYEVIK <sup>H</sup> KL <sup>R</sup> CRGK <sup>C</sup> QKEAKR <sup>S</sup> SA	
mASIC1a	EQKKAYEIA <sup>G</sup> LLGDIGGQMG <sup>L</sup> FIGASILT <sup>V</sup> LELFDYAYEVIK <sup>R</sup> HL <sup>R</sup> CRGK <sup>C</sup> QKEAKR <sup>N</sup> SA	
hASIC1a	DKGVALSLDDV <sup>K</sup> RHN <sup>P</sup> CE <sup>S</sup> LRGHPAGMTYAANILPHHPARGTFEDFT <sup>C</sup>	
mASIC1a	DKGVALSLDDV <sup>K</sup> RHN <sup>P</sup> CE <sup>S</sup> LRGHPAGMTYAANILPHHPARGTFEDFT <sup>C</sup>	

**Supplemental Figure 1. Alignment of human and mouse ASIC1a protein sequences.**

Gray regions indicate the first and second transmembrane region (TM1 and TM2, respectively). The two key positions, 70 and 285, are highlighted in yellow.